

SEQUENCE LISTING

Seq. B1  
SEQ ID NO: 1

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG

40

SEQ ID NO: 2

Sequence Length: 39

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGAGWCAG ACACACTCCT GTTATGGGT

39

SEQ ID NO: 3

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG

40

SEQ ID NO: 4

Sequence Length: 43

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

43

SEQ ID NO: 5

Sequence Length: 40

005227 E255460

**Topology: Linear**

### Sequence.

35

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: \ Single

**Topology:** ~~Linear~~

**Molecular Type:** Synthetic DNA

## Sequence

37

SEQ ID NO: 11

Sequence Length: 38

Sequence Type: Nucleic acid

**Strandedness: Single**

**Topology: Linear**

**Molecular Type:** Synthetic DNA

### Sequence

38

SEQ ID NO: 12

Sequence Length: 27

Sequence Type: Nucleic acid

Strandedness: Single

**Topology: Linear**

**Molecular Type:** Synthetic DNA

## Sequence

27

SEQ ID NO: 13

Sequence Length: 37

**Sequence: Type: Nucleic acid**

**Strandedness: Single**

**Topology: Linear**

**Molecular Type:** Synthetic DNA

## Sequence

37

SEQ ID NO: 14

Sequence Length: 36

Sequence Type: Nucleic acid

Strandedness: Singl

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT

36

SEQ ID NO: 15

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAAGWTGT GCTTAACTG GGTTTTT

37

SEQ ID NO: 16

Sequence Length: 35

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGRACCTTG GGYTCAGCTT GRTTT

35

SEQ ID NO: 17

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGACTCCA GGCTCAATTT AGTTTTCCTT

40

SEQ ID NO: 18

Sequence Length: 37

Sequence Type: Nucleic acid

005321 24554260

Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC	37
SEQ ID NO: 19	
Sequence Length: 36	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT	36
SEQ ID NO: 20	
Sequence Length: 33	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG	33
SEQ ID NO: 21	
Sequence Length: 40	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	
Sequence	
ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCTG	40
SEQ ID NO: 22	
Sequence Length: 37	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	
Molecular Type: Synthetic DNA	

Sequ nc

ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG

37

SEQ ID NO: 23

Sequence Length: 38

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGATTTTG GGCTGATTTT TTTTATTG

38

SEQ ID NO: 24

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGATGCTGT TAAGTCTTCT GTACCTG

37

SEQ ID NO: 25

Sequence Length: 28

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGATCCCGGG CCAGTGGATA GACAGATG

28

SEQ ID NO: 26

Sequence Length: 382

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Original Source

Organism: Mouse

Immediate Source

005221 222444

Features: 1..72 sig peptide  
73..382 mat peptide

## Sequenc

ATG GAG TCA CAT ATT CAG GTC TTT GTA TAC ATG TTG CTG TGG TTG TCT	48
Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser	
5 10 15	
GGT GTT GAT GGA GAC ATT GTG ATG ACC CAG TCT CAA AAA TTC ATG TCC	96
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser	
20 25 30	
ACA TCA GTA GGA GAC AGG GTC AGC GTC ACC TGC AAG GCC AGT CAG AAT	144
Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn	
35 40 45	
GTG GGT ACT AAT GTA GCC TGG TAT CAA CAG AAA CCA GGG CAA TCT CCT	192
Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro	
50 55 60	
AAA CCA CTG ATT TAC TCG GCA TCC TAT CGG TAC AGT GGA GTC CCT GAT	240
Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp	
65 70 75 80	
CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC ACC	288
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr	
85 90 95	
AAT GTG CAG TCT GAA GAC TTG GCA GAC TAT TTC TGT CAG CAA TAT AAC	336
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn	
100 105 110	
AGC TAT CCT CGG GCG TTC GGT GGA GGC ACC AAA CTG GAA ATC AAA C	382
Ser Tyr Pro Arg Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
115 120 125	

SEQ ID NO: 27

Sequence Length: 409

**Sequence Type:** Nucleic acid

**Strandedness: Double**

**Topology:** Linear

Molecular Type: cDNA

Original Source

Organism: Mouse

Immediate Source

Clone: pUC-M21-V<sub>II</sub>

Features: 1..57 sig peptide

58..409 mat peptide

Sequence

ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG	48
Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly	
5 10 15	
GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG	96
Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys	
20 25 30	
CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT	144
Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile	
35 40 45	
AAA GAC ACC TAT ATA CAC TGG GCG AAG CAG AGG CCT GAA CAG GGC CTG	192
Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu	
50 55 60	
GAG TGG ATT GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC	240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp	
65 70 75 80	
CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC	288
Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn	
85 90 95	
ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC	336
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val	
100 105 110	
TAT TAC TGT GCT TCG GCC TAC TAT GTT AAC CAG GAC TAC TCG GGT CAA	384
Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln	
115 120 125	



409

34

34

43

34 .

SEQ ID NO: 32

Sequence Length: 18

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CAGACAGTGG TTCAAAGT

18

SEQ ID NO: 33

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GAATTCGGAT CCACTCACGT TTGATT

26

SEQ ID NO: 34

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC

44

SEQ ID NO: 35

Sequence Length: 38

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG

38

SEQ ID NO: 36

Sequence Length: 47

Sequence Type: Nucleic acid

005221 2554260

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG

47

SEQ ID NO: 37

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC

44

SEQ ID NO: 38

Sequence Length: 47

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG

47

SEQ ID NO: 39

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGATAGCTGT TATATTGCTG GCAGTAGTAG GTAGCGATGT CCTC

44

SEQ ID NO: 40

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

005331 62364650

Organism: Mouse and human  
Immediat Source

Clon : HEF-RVL-M21a-gk  
Amino acid -19--1:leader  
Amino acid 1 - 23:FR1  
Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

## Sequence

ATG GGA TGG AGC TGT ATC	ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile	Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19	15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA ACC ACC CTG AGC GCC	96	
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala		
-1 1	5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144	
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val		
15 20 25		
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192	
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys		
30 35 40		
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240	
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg		
45 50 55 60		
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288	
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser		
65 70 75		

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GCG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 41

Sequence Length: 31

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGTACCGACT ACACCTTCAC CATCAGCAGC C 31

SEQ ID NO: 42

Sequence Length: 31

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGTGAAGGTG TAGTCGGTAC CGCTACCGCT A 31

SEQ ID NO: 43

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21b-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

005221-5237250

~~Amino acid 35 - 49:FR2~~  
~~Amino acid 50 - 56:CDR2~~  
~~Amino acid 57 - 88:FR3~~  
~~Amino acid 89 - 97:CDR3~~  
~~Amino acid 98 - 107:FR4~~

## Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GGT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGT GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 44

Sequence Length: 29

**Sequence Type:** Nucleic acid

Strandedness: Singl  
Topology: Linear  
Mol cular Type: Synth tic DNA  
Sequence

GCTACCTACT TCTGCCAGCA ATATAACAG

29

SEQ ID NO: 45

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGCTGGCAGA AGTAGGTAGC GATGTCCTC

29

SEQ ID NO: 46

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21c-gr

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT

48

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

-19

-15

-10

-5

GTC CAG TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC AOC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 47

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source:

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21d-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

005331 634740



Amino acid 98 - 107:FR4

**Sequence Length: 29**

Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

TGACAGAGTG TCCGTCACCT GTAAGGCCA

29

SEQ ID NO: 49

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TTACAGGTGA CGGACACTCT GTCACCCAC

29

SEQ ID NO: 50

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21e-g\*

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

005221 E2854650

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG ACC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TCG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CCG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 51

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

005221 2455460

Clone: HEF-RVL-M21f-gk  
 Amino acid -19--1:leader  
 Amino acid 1 - 23:FR1  
 Amino acid 24 - 34:CDR1  
 Amino acid 35 - 49:FR2  
 Amino acid 50 - 56:CDR2  
 Amino acid 57 - 88:FR3  
 Amino acid 89 - 97:CDR3  
 Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC CAC ATC CAG ATG ACC CAG AGC CCA AGC ACC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA ACC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA CAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	

005221-22500

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

379

SEQ ID NO: 52

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GACTTCACCT TGACCATCAG CAGCCT

26

SEQ ID NO: 53

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CTGCTGATGG TCAAGGTGAA GTCGGT

26

SEQ ID NO: 54

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21g-gκ

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

005221 2554260

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT GCG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GCG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 55

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

005221 E286h260

Original Source

Organism: Mouse and human

Immediate Source

Clon : HEF-RVL-M21h-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GCA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	

006221-22561260

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
           80                          85                          90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
           95                          100                         105

SEQ ID NO: 56

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCCGCT GATCTACTC 29

SEQ ID NO: 57

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCGGCT TTGGACTCTG TCCTGGCTT 29

SEQ ID NO: 58

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M211-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

006221 E2357450



## Sequence

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1 1 5 10

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40

CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA 240  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
63 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 59

**Sequence Length: 26**

Sequence Type: Nucleic acid

Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

GAGGACATCG CTGACTACTT CTGCCA

26

SEQ ID NO: 60

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA  
Sequence

AAGTAGTCAG CGATGTCCTC TGGCTG

26

SEQ ID NO: 61

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21j-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT

48

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

-19

-15

-10

-5

006221-2257260

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TCC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GCG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 62

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21k-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

006222T E2554260

Amino acid 24 - 34:CDR1  
 Amino acid 35 - 49:FR2  
 Amino acid 50 - 56:CDR2  
 Amino acid 57 - 88:FR3  
 Amino acid 89 - 97:CDR3  
 Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 63

Sequence Length: 379

00749873-12300

Original Source

**Organism:** Mouse and human

Clone: HEF-RVL-M211-gk

Amino acid 98 - 107:FR4

45 50 55 60

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

**Immediate Source**

## Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -13 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CAA AAG TTC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 23	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

379

SEQ ID NO: 67

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCTGCT GATCTACTC

29

SEQ ID NO: 68

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCAGCTT TGGACTCTG TCCTGGCTT

29

SEQ ID NO: 69

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21n-g\*

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

09749873-122900



Amino acid 98 - 107:FR4

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Il Ile Leu Ser L u Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 70

Sequence Length: 379

Sequence Type: Nucleic acid

**Strandedness: Double**

Topology: Linear

**Molecular Type:** Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M210-g\*

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TCG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC ACC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	

005221-1250

336

379

Sequence Length: 23

Sequence Type: Nucleic acid

**Strandedness: Single**

**Topology:** Linear

**Molecular Type:** Synthetic DNA

### Sequence

23

SEQ ID NO: 72

Sequence Length: 23

Sequence Type: Nucleic acid

Strandedness: Single

**Topology:** Linear

**Molecular Type:** Synthetic DNA

## Sequence

23.

SEQ ID NO: 73

Sequence Length: 379

**Sequence Type:** Nucleic acid

**Strandedness: Double**

**Topology: Linear**

**Molecular Type:** Synthetic

### Original Source

**Organism:** Mouse and human

### Immediate Source

**Clone:** HEF-RVL-M21p-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

**Amino acid 24 - 34:CDR1**

## Sequence

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

**Sequence Type:** Nucleic acid

AGGATCAATC CT 132

SEQ ID NO: 78  
Sequence Length: 25  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA

Sequence

GATAAGCTTC CACCATGGAC TGGAC

25

SEQ ID NO: 79  
Sequence Length: 25  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA

Sequence

GTCGGATCCA CTCACCTGAG GAGAC

25

SEQ ID NO: 80  
Sequence Length: 409  
Sequence Type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Molecular Type: Synthetic  
Original Source

Organism: Mouse and human

Immediate Source

Clone: HEP-RVH-M21-gy1  
Amino acid -19--1:leader  
Amino acid 1 - 30:FR1  
Amino acid 31 - 35:CDR1  
Amino acid 36 - 49:FR2  
Amino acid 50 - 66:CDR2  
Amino acid 67 - 98:FR3  
Amino acid 99 - 106:CDR3  
Amino acid 107 - 117:FR4

Sequence

005227-12200

ATG GAC TGG ACC TGG AGG GTC TTC TTC TTG CTG GCT GTA GCT CCA GGT 48  
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly  
-19 -15 -10 -5

GCT CAC TCC CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG GTG AAG AAG 96  
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
-1 1 5 10

CCT GCG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC TTC AAC ATT 144  
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile  
15 20 25

AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA CAG GGC CTG 192  
Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
30 35 40

GAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240  
Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp  
45 50 55 60

CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA TCC ACG AAC 288  
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn  
65 70 75

ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACA GCC TTT 336  
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe  
80 85 90

TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC TGG GGC CAA 384  
Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln  
95 100 105

GGG ACC ACT GTC ACC GTC TCC TCA G 409  
Gly Thr Thr Val Thr Val Ser Ser  
110 115

SEQ ID NO: 81

Sequence Length: 84

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

0074933-122900

Molecular Type: Synth tic DNA

Sequ nce

AGCTTGTCAC CGTCTCCTCA GGTGGTCCTG GTTCGGGTGG TCCTGCTTCG GGTGGTGGCG 60

GATCGGACAT CCAGATGACC CAGG 84

SEQ ID NO: 82

Sequence Length: 84

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AATTCCTGGG CCATCTGGAT GTCCGATCCG CCACCACCCG AACCACCACC ACCCGAACCA 60

CCACCACCTG AGGAGACGGT GACA 84

SEQ ID NO: 83

Sequence Length: 34

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG 34

SEQ ID NO: 84

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CCACCCGAAC CACCACCACC TGAGGAGACG GTGACAGTGG T 41

SEQ ID NO: 85

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

005221-2234760



## Sequence

GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G

41

SEQ ID NO: 86

Sequence Length: 41

Sequence Type: Nucleic acid

**Strandedness: Single**

**Topology: Linear**

**Molecular Type:** Synthetic DNA

## Sequence

GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A

41

SEQ ID NO: 87

Sequence Length: 44

Sequence Type: Nucleic acid

**Strandedness: Single**

**Topology: Linear**

**Molecular Type:** Synthetic DNA

## Sequence

TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG

44

SEQ ID NO: 88

**Sequence Length: 57**

**Sequence Type:** Nucleic acid

**Strandedness: Single**

**Topology: Linear**

**Molecular Type:** Synthetic DNA

## Sequence

CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGGT

57

SEQ ID NO: 89

Sequence Length: 822

**Sequence Type:** Nucleic acid

**Strandedness: Double**

**Topology: Linear**

**Molecular Type:** Synthetic

### Original Source

**Organism:** Mouse and human

### Immediate Source

Clone: pSCFVT7-hm21

Amino acid 1 - 22:leader

Amino acid 23 - 139:H chain V region

Amino acid 140 - 154:Linker

Amino acid 155 - 261:L chain V region

Amino acid 262 - 269:FLAG

Amino acid sequence of Fv polypeptide scFv-hm21 and  
nucleotide sequence coding therefor

Sequence

ATG AAA TAC CTA TTG CCT ACC GCA GCC GCT GGA TTG TTA TTA CTC GCT	48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala	
5 10 15	
GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG	96
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu	
20 25 30	
GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC	144
Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly	
35 40 45	
TTC AAC ATT AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA	192
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly	
50 55 60	
CAG GGC CTG GAG TGG ATG GCA AGG ATT GAT CCT GCG GAT GGT AAT ACT	240
Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr	
65 70 75 80	
AAA TAT GAC CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA	288
Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu	
85 90 95	
TCC ACG AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC	336
Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp	
100 105 110	

006221 22854250

ACA GCC TTT TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC	384
Thr Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr	
115 120 125	
TGG GGC CAA GGG ACC ACT GTC ACC GTC TCC TCA GGT GGT GGT GGT TCG	432
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser	
130 135 140	
GGT GGT GGT GGT TCG GGT GGT GGC GGA TCG GAC ATC CAG ATG ACC CAG	480
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln	
145 150 155 160	
AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC	528
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr	
165 170 175	
TGT AAG GCC AGT CAG AAT GTG GGT ACT AAT GTA GCC TGG TAC CAG CAG	576
Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln	
180 185 190	
AAG CCA GGA AAG GCT CCA AAG CCG CTG ATC TAC TCG GCA TCC TAT CGG	624
Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg	
195 200 205	
TAC AGT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC	672
Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
210 215 220	
TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC	720
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr	
225 230 235 240	
TAC TGC CAG CAA TAT AAC AGC TAT GCT CGG GCG TTC GGC CAA GGG ACC	768
Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr	
245 250 255	
AAG GTC GAA ATC AAA GAC TAC AAA GAC GAT GAC GAT AAA	807
Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys	
260 265	
TAATAAGAAT TCTTG	822

SEQ ID NO: 90

Sequence Length: 45

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Features: Amino acid sequence of linker region of Fv polypeptide  
and nucleotide sequence coding therefor

Sequence

GGT GGT GGT GGT TCG GGT GGT GGT TCG GGT GGT GGC GGA TCG

45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

5

10

15

007493-1229